



SEQUENCE LISTING

<110> KAYANO, Tohru
TANIGUCHI, Mutsuko
YAMAUCHI, Hiroshi
KURIMOTO, Masashi

<120> Antibody specific to interleukin 18 precursor

<130> KAYANO=1.

<150> JP 324,860/99

<151> 1999-11-16

<160> 13

<210> 1

<211> 36

<212> PRT

<213> Homo sapiens

<400> 1

Met Ala Ala Glu Pro Val Glu Asp Asn Cys Ile Asn Phe Val Ala Met
1 5 10 15

Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala Glu Asp Asp Glu Asn
20 25 30

Leu Glu Ser Asp
35

<210> 2

<211> 35

<212> PRT

<213> Mus Musculus

<400> 2

Met Ala Ala Met Ser Glu Asp Ser Cys Val Asn Phe Lys Glu Met Met
1 5 10 15

Phe Ile Asp Asn Thr Leu Tyr Phe Ile Pro Glu Glu Asn Gly Asp Leu
20 25 30

Glu Ser Asp
35

<210> 3

<211> 157

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> (73)

<223> Xaa is Ile or Thr

<400> 3

Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn
1 5 10 15

Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp
20 25 30

Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile
35 40 45

Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile
50 55 60

Ser Val Lys Cys Glu Lys Ile Ser Xaa Leu Ser Cys Glu Asn Lys Ile
65 70 75 80

Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys
85 90 95

Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys
100 105 110

Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu
115 120 125

Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu
130 135 140

Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp
145 150 155

<210> 4
<211> 193
<212> PRT
<213> Homo sapiens

<220>
<221> PROPEP
<222> (-36)...(-1)

<220>
<221> CHAIN
<222> (1)...(157)

<220>
<221> UNSURE
<222> (73)
<223> Xaa is Ile or Thr

<400> 4
Met Ala Ala Glu Pro Val Glu Asp Asn Cys Ile Asn Phe Val Ala Met
-35 -30 -25

Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala Glu Asp Asp Glu Asn
-20 -15 -10 -5

Leu Glu Ser Asp Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile
1 5 10

Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro
 15 20 25
 Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg
 30 35 40
 Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met
 45 50 55 60
 Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Xaa Leu Ser Cys
 65 70 75
 Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile
 80 85 90
 Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly
 95 100 105
 His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe
 110 115 120
 Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys
 125 130 135 140
 Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu
 145 150 155

Asp

<210> 5
 <211> 157
 <212> PRT
 <213> Mus musculus

<220>
 <221> UNSURE
 <222> (70)
 <223> Xaa is Met or Thr

<400> 5
 Asn Phe Gly Arg Leu His Cys Thr Thr Ala Val Ile Arg Asn Ile Asn
 1 5 10 15

Asp Gln Val Leu Phe Val Asp Lys Arg Gln Pro Val Phe Glu Asp Met
 20 25 30

Thr Asp Ile Asp Gln Ser Ala Ser Glu Pro Gln Thr Arg Leu Ile Ile
 35 40 45

Tyr Met Tyr Lys Asp Ser Glu Val Arg Gly Leu Ala Val Thr Leu Ser
 50 55 60

Val Lys Asp Ser Lys Xaa Ser Thr Leu Ser Cys Lys Asn Lys Ile Ile
 65 70 75 80

Ser Phe Glu Glu Met Asp Pro Pro Glu Asn Ile Asp Asp Ile Gln Ser
 85 90 95

Asp Leu Ile Phe Phe Gln Lys Arg Val Pro Gly His Asn Lys Met Glu
100 105 110

Phe Glu Ser Ser Leu Tyr Glu Gly His Phe Leu Ala Cys Gln Lys Glu
115 120 125

Asp Asp Ala Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp
130 135 140

Lys Ser Val Met Phe Thr Leu Thr Asn Leu His Gln Ser
145 150 155

<210> 6
<211> 192
<212> PRT
<213> Mus musculus

<220>
<221> PROPEP
<222> (-35)...(-1)

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<221> CHAIN
<222> (1)...(157)

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<220>
<221> UNSURE
<222> (70)
<223> Xaa is Met or Thr

<400> 6
Met Ala Ala Met Ser Glu Asp Ser Cys Val Asn Phe Lys Glu Met Met
-35 -30 -25 -20

Phe Ile Asp Asn Thr Leu Tyr Phe Ile Pro Glu Glu Asn Gly Asp Leu
-15 -10 -5

Glu Ser Asp Asn Phe Gly Arg Leu His Cys Thr Thr Ala Val Ile Arg
1 5 10

Asn Ile Asn Asp Gln Val Leu Phe Val Asp Lys Arg Gln Pro Val Phe
15 20 25

Glu Asp Met Thr Asp Ile Asp Gln Ser Ala Ser Glu Pro Gln Thr Arg
30 35 40 45

Leu Ile Ile Tyr Met Tyr Lys Asp Ser Glu Val Arg Gly Leu Ala Val
50 55 60

Thr Leu Ser Val Lys Asp Ser Lys Xaa Ser Thr Leu Ser Cys Lys Asn
65 70 75

Lys Ile Ile Ser Phe Glu Glu Met Asp Pro Pro Glu Asn Ile Asp Asp
80 85 90

Ile Gln Ser Asp Leu Ile Phe Phe Gln Lys Arg Val Pro Gly His Asn
95 100 105

Lys Met Glu Phe Glu Ser Ser Leu Tyr Glu Gly His Phe Leu Ala Cys
110 115 120 125

Gln Lys Glu Asp Asp Ala Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu
130 135 140

Asn Gly Asp Lys Ser Val Met Phe Thr Leu Thr Asn Leu His Gln Ser
145 150 155

<210> 7
<211> 582
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(582)

<220>
<221> mat peptide
<222> (109)...(579)

<220>
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<222> (325)...(327)
<223> Xaa is Ile or Thr

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Met Ala Ala Glu Pro Val Glu Asp Asn Cys Ile Asn Phe Val Ala Met
-35 -30 -25

aaa ttt att gac aat acg ctt tac ttt ata gct gaa gat gat gaa aac 96
Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala Glu Asp Asp Glu Asn
-20 -15 -10 -5

ctg gaa tca gat tac ttt ggc aag ctt gaa tct aaa tta tca gtc ata 144
Leu Glu Ser Asp Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile
1 5 10

aga aat ttg aat gac caa gtt ctc ttc att gac caa gga aat cgg cct 192
Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro
15 20 25

cta ttt gaa gat atg act gat tct gac tgt aga gat aat gca ccc cgg 240
Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg
30 35 40

acc ata ttt att ata agt atg tat aaa gat agc cag cct aga ggt atg 288
Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met
45 50 55 60

gct gta act atc tct gtg aag tgt gag aaa att tca ayt ctc tcc tgt 336
Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Xaa Leu Ser Cys
65 70 75

gag aac aaa att att tcc ttt aag gaa atg aat cct cct gat aac atc 384
Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile

80

85

90

aag gat aca aaa agt gac atc ata ttc ttt cag aga agt gtc cca gga 432
 Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly
 95 100 105

cat gat aat aag atg caa ttt gaa tct tca tca tac gaa gga tac ttt 480
 His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe
 110 115 120

cta gct tgt gaa aaa gag aga gac ctt ttt aaa ctg att ttg aaa aaa 528
 Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys
 125 130 135 140

gag gat gaa ttg ggg gat aga tct ata atg ttc act gtt caa aac gaa 576
 Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu
 145 150 155

gac tag 582
 Asp

<210> 8
 <211> 27
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Designed oligonucleotide as a sense primer for PCR to amplify a
 DNA fragment containing a coding sequence for a part of propeptide
 sequence of human IL-18 precursor

<400> 8
 agagatctgc tgctgaacca gtagaag 27

<210> 9
 <211> 45
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Designed oligonucleotide as an antisense primer for PCR to amplify
 a DNA fragment containing a coding sequence for a part of propeptide
 sequence of human IL-18 precursor

<400> 9
 tcaagcttag tgatggtgat ggtgatgac tgattccagg ttttc 45

<210> 10
 <211> 49
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Designed oligonucleotide as a sense primer for PCR to amplify a
 DNA fragment containing a coding sequence for human IL-18 precursor

<400> 10
 ggtagggatc tgtagcagca tgacgataag atggctgctg aaccagtag 49

<210> 11
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Designed oligonucleotide as an antisense primer for PCR to amplify a DNA fragment containing a coding sequence for human IL-18 precursor

<400> 11
tgctcgagtt agtcttcggt ttgaacagtg 30

<210> 12
<211> 47
<212> DNA
<213> Artificial sequence

<220>
<223> Designed oligonucleotide as a sense primer for PCR to amplify a DNA fragment containing a coding sequence for human IL-18 precursor

<400> 12
ggctagcatg actggtggac agcaaatggg tcgggatctg tacgacg 47

a.
<210> 13
<211> 579
<212> DNA
<213> Mus musculus

Sub
P.
<220>
<221> CDS
<222> (1)... (579)

<220>
<221> mat peptide
<222> (106)... (576)

<220>
<221> UNSURE
<222> (313)... (315)
<223> Xaa is Met or Thr

<400> 13
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Met Ala Ala Met Ser Glu Asp Ser Cys Val Asn Phe Lys Glu Met Met
-35 -30 -25 -20

ttt att gac aac acg ctt tac ttt ata cct gaa gaa aat gga gac ctg 96
Phe Ile Asp Asn Thr Leu Tyr Phe Ile Pro Glu Glu Asn Gly Asp Leu
-15 -10 -5

gaa tca gac aac ttt ggc cga ctt cac tgt aca acc gca gta ata cgg 144
Glu Ser Asp Asn Phe Gly Arg Leu His Cys Thr Thr Ala Val Ile Arg
1 5 10

aat ata aat gac caa gtt ctc ttc gtt gac aaa aga cag cct gtg ttc 192
Asn Ile Asn Asp Gln Val Leu Phe Val Asp Lys Arg Gln Pro Val Phe

15

20

25

gag gat atg act gat att gat caa agt gcc agt gaa ccc cag acc aga 240
 Glu Asp Met Thr Asp Ile Asp Gln Ser Ala Ser Glu Pro Gln Thr Arg
 30 35 40 45

ctg ata ata tac atg tac aaa gac agt gaa gta aga gga ctg gct gtg 288
 Leu Ile Ile Tyr Met Tyr Lys Asp Ser Glu Val Arg Gly Leu Ala Val
 50 55 60

acc ctc tct gtg aag gat agt aaa ayg tct acc ctc tcc tgt aag aac 336
 Thr Leu Ser Val Lys Asp Ser Lys Xaa Ser Thr Leu Ser Cys Lys Asn
 65 70 75

aag atc att tcc ttt gag gaa atg gat cca cct gaa aat att gat gat 384
 Lys Ile Ile Ser Phe Glu Glu Met Asp Pro Pro Glu Asn Ile Asp Asp
 80 85 90

ata caa agt gat ctc ata ttc ttt cag aaa cgt gtt cca gga cac aac 432
 Ile Gln Ser Asp Leu Ile Phe Phe Gln Lys Arg Val Pro Gly His Asn
 95 100 105

aag atg gag ttt gaa tct tca ctg tat gaa gga cac ttt ctt gct tgc 480
 Lys Met Glu Phe Glu Ser Ser Leu Tyr Glu Gly His Phe Leu Ala Cys
 110 115 120 125

caa aag gaa gat gat gct ttc aaa ctc att ctg aaa aaa aag gat gaa 528
 Gln Lys Glu Asp Asp Ala Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu
 130 135 140

aat ggg gat aaa tct gta atg ttc act ctc act aac tta cat caa agt 576
 Asn Gly Asp Lys Ser Val Met Phe Thr Leu Thr Asn Leu His Gln Ser
 145 150 155

tag

579